



SEQUENCE LISTING

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Auge, Jennifer Stoehr
Ohlendorf, Douglas

<120> MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE

<130> 600.346USWO

<140> US 09/308,830

<141> 1999-08-04

<150> PCT/US97/22228

<151> 1997-12-05

<150> US 60/032,930

<151> 1996-12-06

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<170> PatentIn version 3.1

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Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln Asp Pro Asp	
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cca agc caa ctt cac aga tct agt tta gtt aaa aac ctt caa aat ata	980
Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu Gln Asn Ile	
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Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn Val Lys Ser	
55 60 65	
gtt gat caa ctt tta tct cac cat tta ata tat aat gtt tca ggg cca	1076
Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val Ser Gly Pro	
70 75 80	
aat tat gat aaa tta aaa act gaa ctt aag aac caa gag atg gca act	1124
Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu Met Ala Thr	
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Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu Tyr Tyr His	
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ctc tgt tat tta tgt gaa aat gca gaa agg agt gca tgt atc tac gga	1220
Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys Ile Tyr Gly	
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Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro Lys Lys Ile	
135 140 145	
gtc gtt aaa gta tca atc gat ggt atc caa agc cta tca ttt gat att	1316
Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser Phe Asp Ile	
150 155 160	
gaa aca aat aaa aaa atg gta act gct caa gaa tta gac tat aaa gtt	1364
Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp Tyr Lys Val	
165 170 175	

aga aaa tat ctt aca gat aat aag caa cta tat act aat gga cct tct 1412
 Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn Gly Pro Ser
 180 185 190 195

aaa tat gaa act gga tat ata aag ttc ata cct aag aat aaa gaa agt 1460
 Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn Lys Glu Ser
 200 205 210

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 Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln Ser Lys Tyr
 215 220 225

ctt atg ata tat aaa gat aat gaa acg ctt gac tca aac aca agc caa 1556
 Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn Thr Ser Gln
 230 235 240

att gaa gtc tac cta aca acc aag taactttttg cttttggcaa ccttacctac 1610
 Ile Glu Val Tyr Leu Thr Thr Lys
 245 250

tgctggattt agaaatttta ttgcaattct tttattaatg taaaaaccgc tcatttgatg 1670

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Asp Pro Asp Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu
 35 40 45

Gln Asn Ile Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn
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Val Lys Ser Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val
 65 70 75 80

Ser Gly Pro Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu

85

90

95

Met Ala Thr Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu
 100 105 110

Tyr Tyr His Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys
 115 120 125

Ile Tyr Gly Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro
 130 135 140

Lys Lys Ile Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser
 145 150 155 160

Phe Asp Ile Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp
 165 170 175

Tyr Lys Val Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn
 180 185 190

Gly Pro Ser Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn
 195 200 205

Lys Glu Ser Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln
 210 215 220

Ser Lys Tyr Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn
 225 230 235 240

Thr Ser Gln Ile Glu Val Tyr Leu Thr Thr Lys
 245 250